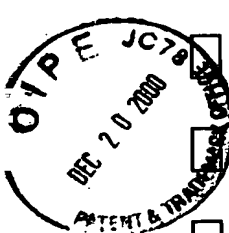


**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 
- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: Both the paper copy and the computer readable form of the "Sequence Listing" fail to properly list the sequences depicted in Fig. 1C. The sequences purported to list these sequences, i.e. SEQ ID NOs: 7 and 8, do not find support in the specification as filed.

**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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# SEQUENCE LISTING

15/C  
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<110> LONGACRE-ANDRE, SHIRLEY  
ROTH, CHARLES  
BARNWELL, JOHN  
MENDIS, KAMINI  
NATO, FARIDABANO

<120> RECOMBINANT PROTEIN CONTAINING A C-TERMINAL FRAGMENT OF  
PLASMODIUM MSP-1

<130> 0660-0139-OXPCT

<140> 09/125,031

<141> 1999-03-10

<150> PCT/FR97/00290

<151> 1997-02-14

<150> FR96/01822

<151> 1996-02-14

<160> 15

<170> PatentIn Ver. 2.1

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<211> 291

<212> DNA

<213> Artificial Sequence

<220>

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1				5					10					15		

aac	tct	ggc	tgt	ttc	aga	cac	ttg	gac	gag	aga	gag	gag	tgt	aaa	tgt	96
Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	
			20					25					30			

ctg	ctg	aac	tac	aaa	cag	gag	ggc	gac	aag	tgc	gtg	gag	aac	ccc	aac	144
Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn	
			35				40						45			

ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc	192
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys	
50 55 60	
acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt	240
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys	
65 70 75 80	
acc aaa ccc gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc taa	288
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser	
85 90 95	
taa	291

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Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn	
35 40 45	
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys	
50 55 60	
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys	
65 70 75 80	
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser	
85 90 95	

<210> 3  
 <211> 279  
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tgtgttgaaa atccaaatcc tacttgtaac gaaaataatg gtggatgtga tgcagatgcc	180
aatgtaccg aagaagattc aggtagcaac ggaaagaaaa tcacatgtga atgtactaaa	240
cctgattcctt atccactttt cgatgggtatt ttctgcagt	279

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<210> 4  
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<212> DNA  
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1 5 10 15  
  
aac tct ggc tgt ttc aga cac ttg gac gag aga gag gag tgt aaa tgt 96  
Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys  
20 25 30  
  
ctg ctg aac tac aaa cag gag ggc gac aag tgc gtg gag aac ccc aac 144  
Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn  
35 40 45  
  
ccg acc tgt aac gag aac aac ggc ggc tgt gac gca gac gcc aaa tgc 192  
Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys  
50 55 60  
  
acc gag gag gac tcg ggc agc aac ggc aag aaa atc acg tgt gag tgt 240  
Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys  
65 70 75 80  
  
acc aaa ccc gac tcg tac ccg ctg ttc gac ggc atc ttc tgc agc tcc 288  
Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser Ser  
85 90 95  
  
tct aac ttc ttg ggc atc tcg ttc ttg ttg atc ctc atg ttg atc ttg 336  
Ser Asn Phe Leu Gly Ile Ser Phe Leu Leu Ile Leu Met Leu Ile Leu  
100 105 110  
  
tac agc ttc att taa taa 354  
Tyr Ser Phe Ile  
115

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<212> PRT  
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Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys
		20						25					30		
Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn
		35					40					45			
Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys
	50					55					60				
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys
65					70					75					80
Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	Cys	Ser	Ser
				85					90				95		
Ser	Asn	Phe	Leu	Gly	Ile	Ser	Phe	Leu	Leu	Ile	Leu	Met	Leu	Ile	Leu
			100					105					110		
Tyr	Ser	Phe	Ile												
			115												

<210> 6  
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 <212> DNA  
 <213> Plasmodium falciparum

<400> 6

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tgtgttgaaa	atccaaatcc	tacttgtaac	gaaaataatg	gtggatgtga	tgcatatgcc	180
aatgtaccg	aagaagattc	aggtagcaac	ggaaagaaaa	tcacatgtga	atgtactaaa	240
cctgattctt	atccactttt	cgatgggtatt	ttctgcagtt	cctctaactt	cttaggaata	300
tcattcttat	taatactcat	gttaatatata	tacagtttca	tt		342

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 <213> Plasmodium falciparum

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 <222> (1)..(387)

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Met	Lys	Ala	Leu	Leu	Phe	Leu	Phe	Ser	Phe	Ile	Phe	Phe	Val	Thr	Lys	
1				5					10					15		
tgt	caa	tgt	gaa	aca	gaa	agt	tat	aag	cag	ctt	gta	gcc	aac	gtg	gac	96
Cys	Gln	Cys	Glu	Thr	Glu	Ser	Tyr	Lys	Gln	Leu	Val	Ala	Asn	Val	Asp	
			20					25					30			
gaa	ttc	aac	atc	tcg	cag	cac	caa	tgc	gtg	aaa	aaa	caa	tgt	ccc	gag	144
Glu	Phe	Asn	Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln	Cys	Pro	Glu	
		35					40					45				
aac	tct	ggc	tgt	ttc	aga	cac	ttg	gac	gag	aga	gag	gag	tgt	aaa	tgt	192
Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	
	50					55				60						
ctg	ctg	aac	tac	aaa	cag	gag	ggc	gac	aag	tgc	gtg	gag	aac	ccc	aac	240
Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn	
65					70				75					80		
ccg	acc	tgt	aac	gag	aac	aac	ggg	ggc	tgt	gac	gca	gac	gcc	aaa	tgc	288
Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys	
			85					90						95		
acc	gag	gag	gac	tcg	ggc	agc	aac	ggg	aag	aaa	atc	acg	tgt	gag	tgt	336
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys	
			100					105					110			
acc	aaa	ccc	gac	tcg	tac	ccg	ctg	ttc	gac	ggc	atc	ttc	tgc	agc	taa	384
Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	Cys	Ser		
		115					120					125				
taa																387

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<211> 127

<212> PRT

<213> Plasmodium falciparum

<400> 8

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Cys	Gln	Cys	Glu	Thr	Glu	Ser	Tyr	Lys	Gln	Leu	Val	Ala	Asn	Val	Asp	
			20					25					30			
Glu	Phe	Asn	Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln	Cys	Pro	Glu	
		35				40						45				
Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	
	50					55				60						

Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn
65					70					75					80
Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys
			85						90					95	
Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys
			100					105					110		
Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	Cys	Ser	
		115					120					125			

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<211> 330

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<213> Plasmodium falciparum

<220>

<221> CDS

<222> (1)..(330)

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1				5					10					15		

atc	tcg	cag	cac	caa	tgc	gtg	aaa	aaa	caa	tgt	ccc	gag	aac	tct	ggc	96
Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln	Cys	Pro	Glu	Asn	Ser	Gly	
			20				25						30			

tgt	ttc	aga	cac	ttg	gac	gag	aga	gag	gag	tgt	aaa	tgt	ctg	ctg	aac	144
Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	Cys	Lys	Cys	Leu	Leu	Asn	
		35					40					45				

tac	aaa	cag	gag	ggc	gac	aag	tgc	gtg	gag	aac	ccc	aac	ccg	acc	tgt	192
Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	Asn	Pro	Asn	Pro	Thr	Cys	
	50					55					60					

aac	gag	aac	aac	ggc	ggc	tgt	gac	gca	gac	gcc	aaa	tgc	acc	gag	gag	240
Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	Ala	Lys	Cys	Thr	Glu	Glu	
65				70						75					80	

gac	tcg	ggc	agc	aac	ggc	aag	aaa	atc	acg	tgt	gag	tgt	acc	aaa	ccc	288
Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	Cys	Glu	Cys	Thr	Lys	Pro	
				85					90					95		

gac	tcg	tac	ccg	ctg	ttc	gac	ggc	atc	ttc	tgc	agc	taa	taa			330
Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	Cys	Ser					
			100					105					110			

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           20                  25                  30  
 Cys Phe Arg His Leu Asp Glu Arg Glu Glu Cys Lys Cys Leu Leu Asn  
           35                  40                  45  
 Tyr Lys Gln Glu Gly Asp Lys Cys Val Glu Asn Pro Asn Pro Thr Cys  
       50                  55                  60  
 Asn Glu Asn Asn Gly Gly Cys Asp Ala Asp Ala Lys Cys Thr Glu Glu  
   65                  70                  75                  80  
 Asp Ser Gly Ser Asn Gly Lys Lys Ile Thr Cys Glu Cys Thr Lys Pro  
           85                  90                  95  
 Asp Ser Tyr Pro Leu Phe Asp Gly Ile Phe Cys Ser  
           100                  105

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           20                  25                  30  
 Ala Gly Met Tyr Lys Thr Ile Lys Lys Pro Leu Glu Asn His Val Asn  
       35                  40                  45



Ala	Leu	Asn	Thr	Asn	Ile	Ile	Asp	Met	Leu	Asp	Ser	Arg	Leu	Lys	Lys	50	55	60
Arg	Asn	Tyr	Phe	Leu	Asp	Val	Leu	Asn	Ser	Asp	Leu	Asn	Pro	Tyr	Ser	65	70	75
Ile	Pro	His	Ser	Gly	Glu	Tyr	Ile	Ile	Lys	Asp	Pro	Tyr	Lys	Leu	Leu	85	90	95
Asp	Leu	Glu	Lys	Lys	Lys	Leu	Leu	Gly	Ser	Tyr	Lys	Tyr	Ile	Gly	Ala	100	105	110
Ser	Val	Asp	Lys	Asp	Met	Val	Thr	Ala	Asn	Asp	Gly	Leu	Ala	Tyr	Tyr	115	120	125
Gln	Lys	Met	Gly	Asp	Leu	Tyr	Lys	Lys	His	Leu	Asp	Glu	Val	Asn	Ala	130	135	140
Cys	Ile	Lys	Glu	Val	Glu	Ala	Asn	Ile	Asn	Lys	His	Asp	Glu	Glu	Ile	145	150	155
Lys	Lys	Ile	Gly	Ser	Glu	Ala	Ser	Lys	Ala	Asn	Asp	Lys	Asn	Gln	Leu	165	170	175
Asn	Ala	Lys	Lys	Glu	Glu	Leu	Gln	Lys	Tyr	Leu	Pro	Phe	Leu	Ser	Ser	180	185	190
Ile	Gln	Lys	Glu	Tyr	Ser	Thr	Leu	Val	Asn	Lys	Val	His	Ser	Tyr	Thr	195	200	205
Asp	Thr	Leu	Lys	Lys	Ile	Ile	Asn	Asn	Cys	Gln	Ile	Glu	Lys	Lys	Glu	210	215	220
Thr	Glu	Thr	Ile	Val	Asn	Lys	Leu	Glu	Asp	Tyr	Ser	Lys	Met	Asp	Glu	225	230	235
Glu	Leu	Asp	Val	Tyr	Lys	Gln	Ser	Lys	Lys	Glu	Asp	Asp	Val	Lys	Ser	245	250	255
Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Asn	Ser	Lys	Leu	Ile	Asn	Gln	Glu	260	265	270
Glu	Ser	Lys	Lys	Ala	Leu	Ser	Glu	Leu	Leu	Asn	Val	Gln	Thr	Gln	Met	275	280	285
Leu	Asn	Met	Ser	Ser	Glu	His	Arg	Cys	Ile	Asp	Thr	Asn	Val	Pro	Glu	290	295	300
Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp	Gly	Thr	Glu	Glu	Trp	Arg	Cys			

305		310		315		320									
Leu	Leu	Tyr	Phe	Lys	Glu	Asp	Ala	Gly	Lys	Cys	Val	Pro	Ala	Pro	Asn
				325					330					335	
Met	Thr	Cys	Lys	Asp	Lys	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu	Cys
			340					345					350		
Lys	Met	Asn	Asp	Lys	Asn	Glu	Ile	Val	Cys	Lys	Cys	Thr	Lys	Glu	Gly
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35 40 45
Ala Phe Asn Thr Asn Ile Thr Asp Met Leu Asp Ser Arg Leu Lys Lys
50 55 60
Arg Asn Tyr Phe Leu Glu Val Leu Asn Ser Asp Leu Asn Pro Phe Lys
65 70 75 80
Tyr Ser Pro Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys Leu Leu

85

90

95

Asp	Leu	Glu	Lys	Lys	Lys	Lys	Leu	Leu	Gly	Ser	Tyr	Lys	Tyr	Ile	Gly
			100					105					110		
Ala	Ser	Ile	Asp	Lys	Asp	Leu	Ala	Thr	Ala	Asn	Asp	Gly	Val	Thr	Tyr
		115					120					125			
Tyr	Asn	Lys	Met	Gly	Glu	Leu	Tyr	Lys	Thr	His	Leu	Thr	Ala	Val	Asn
	130					135					140				
Glu	Glu	Val	Lys	Lys	Val	Glu	Ala	Asp	Ile	Lys	Ala	Glu	Asp	Asp	Lys
145					150					155					160
Ile	Lys	Lys	Ile	Gly	Ser	Asp	Ser	Thr	Lys	Thr	Thr	Glu	Lys	Thr	Gln
				165					170					175	
Ser	Met	Ala	Lys	Lys	Ala	Glu	Leu	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn
			180					185					190		
Ser	Leu	Gln	Lys	Glu	Tyr	Glu	Ser	Leu	Val	Ser	Lys	Val	Asn	Thr	Tyr
		195					200					205			
Thr	Asp	Asn	Leu	Lys	Lys	Val	Ile	Asn	Asn	Cys	Gln	Leu	Glu	Lys	Lys
	210					215					220				
Glu	Ala	Glu	Ile	Thr	Val	Lys	Lys	Leu	Gln	Asp	Tyr	Asn	Lys	Met	Asp
225					230					235					240
Glu	Lys	Leu	Glu	Glu	Tyr	Lys	Lys	Ser	Glu	Lys	Lys	Asn	Glu	Val	Lys
				245					250					255	
Ser	Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Lys	Ser	Lys	Leu	Ile	Lys	Glu
			260					265					270		
Asn	Glu	Ser	Lys	Glu	Ile	Leu	Ser	Gln	Leu	Leu	Asn	Val	Gln	Thr	Gln
		275					280					285			
Leu	Leu	Thr	Met	Ser	Ser	Glu	His	Thr	Cys	Ile	Asp	Thr	Asn	Val	Pro
	290					295					300				
Asp	Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp	Gly	Thr	Glu	Glu	Trp	Arg
305					310					315					320
Cys	Leu	Leu	Thr	Phe	Lys	Glu	Glu	Gly	Gly	Lys	Cys	Val	Pro	Ala	Ser
				325					330					335	
Asn	Val	Thr	Cys	Lys	Asp	Asn	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu
			340					345					350		

Cys Lys Met Thr Asp Ser Asn Lys Ile Val Cys Lys Cys Thr Lys Glu  
 355 360 365

Gly Ser Glu Pro Leu Phe Glu Gly Val Phe Cys Ser  
 370 375 380

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<211> 380

<212> PRT

<213> Plasmodium vivax-like sp.

<220>

<223> Amino Acids 1-140-REGION I

<220>

<223> Amino Acids 141-178-REGION II

<220>

<223> Amino Acids 179-283-REGION III

<220>

<223> Amino Acids 284-380-REGION IV

<400> 13

Asp Gln Val Thr Thr Gly Glu Ala Glu Ser Glu Ala Pro Glu Ile Leu  
 1 5 10 15

Val Pro Ala Gly Ile Ser Asp Tyr Asp Val Val Tyr Leu Lys Pro Leu  
 20 25 30

Ala Gly Met Tyr Lys Thr Ile Lys Lys Gln Leu Glu Asn His Val Asn  
 35 40 45

Ala Phe Asn Thr Asn Ile Thr Asp Met Leu Asp Ser Arg Leu Lys Lys  
 50 55 60

Arg Asn Tyr Phe Leu Glu Val Leu Asn Ser Asp Leu Asn Pro Phe Lys  
 65 70 75 80

Tyr Ser Ser Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys Leu Leu  
 85 90 95

Asp Leu Glu Lys Lys Lys Lys Leu Ile Gly Ser Tyr Lys Tyr Ile Gly  
 100 105 110

Ala Ser Ile Asp Met Asp Leu Ala Thr Ala Asn Asp Gly Val Thr Tyr  
 115 120 125

Tyr	Asn	Lys	Met	Gly	Glu	Leu	Tyr	Lys	Thr	His	Leu	Asp	Gly	Val	Lys
130						135					140				
Thr	Glu	Ile	Lys	Lys	Val	Glu	Asp	Asp	Ile	Lys	Lys	Gln	Asp	Glu	Glu
145					150					155					160
Leu	Lys	Lys	Leu	Gly	Asn	Val	Asn	Ser	Gln	Asp	Ser	Lys	Lys	Asn	Glu
				165					170					175	
Phe	Ile	Ala	Lys	Lys	Ala	Glu	Leu	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn
			180					185					190		
Ser	Leu	Gln	Lys	Glu	Tyr	Glu	Ser	Leu	Val	Ser	Lys	Val	Asn	Thr	Tyr
		195					200					205			
Thr	Asp	Asn	Leu	Lys	Lys	Val	Ile	Asn	Asn	Cys	Gln	Leu	Glu	Lys	Lys
	210					215					220				
Glu	Ala	Glu	Ile	Thr	Val	Lys	Lys	Leu	Gln	Asp	Tyr	Asn	Lys	Met	Asp
225					230					235					240
Glu	Lys	Leu	Glu	Glu	Tyr	Lys	Lys	Ser	Glu	Lys	Lys	Asn	Glu	Val	Lys
				245					250					255	
Ser	Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Lys	Ser	Lys	Leu	Ile	Lys	Glu
			260					265					270		
Asn	Glu	Ser	Lys	Glu	Ile	Leu	Ser	Gln	Leu	Leu	Asn	Val	Gln	Thr	Gln
		275					280					285			
Leu	Leu	Thr	Met	Ser	Ser	Glu	His	Thr	Cys	Ile	Asp	Thr	Asn	Val	Pro
	290					295					300				
Asp	Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp	Gly	Thr	Glu	Glu	Trp	Arg
305					310					315					320
Cys	Leu	Leu	Thr	Phe	Lys	Glu	Glu	Gly	Gly	Lys	Cys	Val	Pro	Ala	Ser
				325					330					335	
Asn	Val	Thr	Cys	Lys	Asp	Asn	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu
			340					345					350		
Cys	Lys	Met	Thr	Asp	Ser	Asn	Lys	Ile	Val	Cys	Lys	Cys	Thr	Lys	Glu
		355					360					365			
Gly	Ser	Glu	Pro	Leu	Phe	Glu	Gly	Val	Phe	Cys	Ser				
	370					375					380				

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 <211> 281  
 <212> PRT  
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:ALIGNMENT

<220>  
 <223> Amino Acids 1-115-REGION I

<220>  
 <223> Amino Acids 116-125-REGION II

<220>  
 <223> Amino Acids 126-197-REGION III

<220>  
 <223> Amino Acids 198-281-REGION IV

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 Asp Gln Val Thr Thr Gly Glu Ala Glu Ser Glu Ala Pro Glu Ile Val  
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 Pro Gly Ile Tyr Asp Val Val Tyr Lys Pro Leu Ala Gly Met Tyr Lys  
                     20                    25                    30  
 Thr Ile Lys Lys Leu Glu Asn His Val Asn Ala Asn Thr Asn Ile Asp  
             35                    40                    45  
 Met Leu Asp Ser Ala Leu Lys Lys Ala Asn Tyr Phe Leu Val Leu Asn  
     50                    55                    60  
 Ser Asp Leu Asn Pro Ser Gly Glu Tyr Ile Ile Lys Asp Pro Tyr Lys  
     65                    70                    75                    80  
 Leu Leu Asp Leu Glu Lys Lys Lys Leu Gly Ser Tyr Lys Tyr Ile Gly  
             85                    90                    95  
 Ala Ser Asp Asp Thr Ala Asn Asp Gly Tyr Tyr Lys Met Gly Leu Tyr  
             100                    105                    110  
 Lys His Leu Val Lys Val Glu Ile Asp Lys Lys Gly Lys Ala Lys Lys  
             115                    120                    125  
 Glu Leu Lys Tyr Leu Pro Phe Leu Ser Gln Lys Glu Tyr Leu Val Lys  
     130                    135                    140  
 Val Tyr Thr Asp Leu Lys Lys Ile Asn Asn Cys Gln Glu Lys Lys Glu

145					150					155					160
Glu	Val	Lys	Leu	Asp	Tyr	Lys	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Lys	Val
				165					170					175	
Lys	Ser	Ser	Gly	Leu	Leu	Glu	Lys	Leu	Met	Ser	Lys	Leu	Ile	Glu	Ser
			180					185					190		
Lys	Leu	Ser	Leu	Leu	Asn	Val	Gln	Thr	Gln	Leu	Met	Ser	Ser	Glu	His
		195					200					205			
Cys	Ile	Asp	Thr	Asn	Val	Pro	Asn	Ala	Ala	Cys	Tyr	Arg	Tyr	Leu	Asp
	210					215					220				
Gly	Thr	Glu	Glu	Trp	Arg	Cys	Leu	Leu	Phe	Lys	Glu	Gly	Lys	Cys	Val
225					230					235					240
Pro	Ala	Asn	Thr	Cys	Lys	Asp	Asn	Gly	Gly	Cys	Ala	Pro	Glu	Ala	Glu
				245					250					255	
Cys	Lys	Met	Asp	Asn	Ile	Val	Cys	Lys	Cys	Thr	Lys	Glu	Gly	Ser	Glu
			260					265					270		
Pro	Leu	Phe	Glu	Gly	Val	Phe	Cys	Ser							
		275					280								

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<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:peptide

<400> 15

Leu	Asn	Val	Gln	Thr	Gln
1				5	